

REMARKS**1. Status of the Claims and Formal Matters****a. Amendments**

Claims 1-20 are pending in this application. Claims 1-20 are hereby cancelled without prejudice to pursuing these claims in a continuing application. Claims 21-31 are new. Upon entry of these amendments, claims 21-31 are pending and under active consideration. Applicants respectfully request entry of the amendments and remarks made herein into the file history of the present application.

New claim 21 recites a nucleic acid consisting of 18 to 120 nucleotides, support for which may be found throughout the application including claims 1-3 as originally filed. New claim 21 also recites that the sequence of the nucleic acid may comprise (a) at least 18 consecutive nucleotides of SEQ ID NOS: 37404, 37418 or 37429, support for which may be found throughout the application including at Table 1 lines 10,279-10,284, 10,286-10,292, and 10,293-10,299, claim 1, and ¶¶ 20,719, 20,733 and 20,747 of the application as originally filed; (b) an RNA equivalent of (a), support for which may be found at claim 1 and ¶¶ 20,720, 20,734 and 20,748 of the application as originally filed; (c) a sequence at least 46/78 identical to (a) or (b), support for which may be found at claim 1 as originally filed and at Table 1, lines 10,293-10,299 which shows that (i) the sequence of SEQ ID NO: 37429, of which the first half is a partial inverse of its second half as shown in ¶ 20,748 of the application as filed, is 78 nucleotides in length; and (ii) within the predicted hairpin formed by the nucleic acid of SEQ ID NO: 37429, 46 complementary nucleotides are paired; or (d) the complement of any one of (a)-(c), support for which may be found at claim 1 and ¶¶ 20,720, 20,734, and 20,748 of the application as originally filed.

New claim 22 recites the nucleic acid of claim 21 comprising a sequence selected from the following: SEQ ID NOS: 37405, 37419 or 37430, support for which can be found at Table 1 lines 10,279-10,284, 10,286-10,292, and 10,293-10,299, claim 1, and ¶¶ 20,721, 20,735 and 20,749 of the application as originally filed.

New claim 23 recites a nucleic acid with a sequence consisting of (a) SEQ ID NOS: 37404, 37418 or 37429; (b) an RNA equivalent of (a); (c) a sequence at least 46/78 identical to

(a) or (b); or (d) the complement of any one of (a)-(c), support for which may be found throughout the application including at new claim 21.

New claim 24 recites that the nucleic acid of claim 21 consists of 18 to 24 nucleotides, support for which may be found at claims 1-3 as originally filed.

New claim 25 recites that the nucleic acid of claim is an RNA, support for which may be found throughout the application including at claim 1 as originally filed.

New claim 26 recites that the nucleic acid of claim 25 is capable of modulating expression of a target gene, support for which may be found at claim 3 as originally filed.

New claim 27 recites that the nucleic acid of 26 is (a) at least 15/24 complementary to a binding site sequence of 18 to 24 nucleotides of a target gene, support for which can be found at Table 2 lines 199,958-200,017, which shows that among all listed target binding sites of the nucleotide represented by SEQ ID NO: 37405, the sequence of which is included in the sequence of SEQ ID NO: 37404, at the lowest level of complementarity a target binding site of 24 nucleotides has 15 nucleotides complementary to the sequence of SEQ ID NO: 37405; and (b) that the binding site sequence is located in an untranslated region of RNA encoded by the target gene, support for which can be found at ¶¶ 21, 20,723, 20,737, and 20,751 of the specification as originally filed.

New claim 28 recites a vector comprising an HCMV nucleic acid wherein the HCMV nucleic acid consists of the nucleic acid of claim 21, support for which can be found at ¶ 23 of the application as originally filed.

New claim 29 recites a probe comprising an HCMV nucleic acid, wherein the HCMV nucleic acid consists of the nucleic acid of claim 21, support for which can be found at ¶ 27 of the application as originally filed.

New claim 30 recites a gene expression inhibition system comprising the vector of claim 28 and a means for inserting said vector into a cell, support for which can be found at ¶¶ 24-26 of the application as originally filed.

New claim 31 recites a gene expression detection system comprising the probe of claim 29 and a gene expression detector functional to selectively detect expression of at least one gene, support for which can be found at ¶¶ 28-29 of the application as originally filed.

b. Elections/Restrictions

Groups I-VII

At pages 2-4 of the Office Action, the Examiner requires restriction to one of the following inventions under 35 U.S.C. 121:

- I. Claims 1-8, 11, 12 and 14 drawn to a bioinformatically detectable novel viral gene, a probe comprising said novel gene, a vector comprising said novel gene, a kit comprising said vector and a vector inserter and a kit comprising said probe and a gene expression detector.
- II. Claims 9-10, drawn to a method of inhibiting translation of at least one gene comprising introducing the vector of claim 10 into a cell..
- III. Claim 13, drawn to a method of detecting expression using a DNA probe that comprises a bioinformatically detectable novel gene.
- IV. Claims 15-16, drawn to an antiviral substance capable of neutralizing RNA comprising complementarily binding the RNA.
- V. Claim 15 and 17, drawn to an antiviral substance capable of neutralizing RNA comprising immunologically neutralizing RNA.
- VI. Claim 19, drawn to a method of anti-viral treatment comprising neutralizing RNA comprising synthesizing, transfecting and complementarily binding RNA.
- VII. Claim 20, drawn to a method of anti-viral treatment comprising neutralizing RNA comprising immunologically neutralizing RNA.

Applicant elect without traverse Group I, which now is considered claims 21-31, drawn to a bioinformatically detectable novel viral gene, a probe comprising said novel gene, a vector comprising said novel gene, a kit comprising said vector and a vector inserter and a kit comprising said probe and a gene expression detector.

c. Sequence Election Requirement

At page 14 of the Office Action, the Examiner requires restriction to a single nucleic acid sequence under MPEP 803.04. Applicant elects with traverse nucleic acids related to SEQ ID NO: 37404 for further prosecution.

(1) Traversal – Up to Ten Nucleic Acid Sequences Reasonable

The Examiner is permitted under 35 U.S.C. 121 to issue a restriction requirement between independent and distinct inventions. However, the Director has partially waived the requirements of 37 C.F.R. § 1.141 *et seq.* to permit a reasonable number of nucleotide sequences

to be claimed in a single application. *See* Examination of Patent Applications Containing Nucleotide Sequence, 1192 O.G. 68 (November 19, 1996). It has been determined that normally ten sequences constitute a reasonable number for examination purposes absent an exceptional case. *See* MPEP 803.04.

The Examiner has failed to demonstrate that the claimed sequences are an exceptional case necessitating that the number of sequences to be selected be less than ten. Applicant respectfully submits that the Examiner is impermissibly disregarding the waiver of 37 C.F.R. § 1.141 *et seq.* Accordingly, Applicant respectfully requests reconsideration of the restriction requirement and the opportunity to elect ten sequences for further prosecution.

(2) Traversal – SEQ ID NOS: 37404, 37418 and 37429 are Related

Notwithstanding the remarks above, Applicant respectfully requests that SEQ ID NOS: 37418 and 37429 be examined along with SEQ ID NO: 37404. VGR4097 is a Viral Genome Record viral gene which is located on the plus strand of HCMV at an intergenic location between viral genes HHV5gp124 and HHV5gp125. This viral gene encodes at least three hairpins, including SEQ ID NOS: 37404, 37418, and 37429, with these three hairpins clustered within ~1,000 nucleotides of each other. Furthermore, the hairpins of SEQ ID NOS: 37404 and 37418 have similar expression profiles. In view of SEQ ID NOS: 37404, 37418, and 37429 being related by virtue of being encoded by the same polycistronic viral gene, Applicant respectfully requests that SEQ ID NOS: 37418 and 37429 be examined along with SEQ ID NO: 37404.

2. Conclusion

Applicant respectfully submits that the instant application is in good and proper order for allowance and early notification to this effect is solicited. If, in the opinion of the Examiner, a telephone conference would expedite prosecution of the instant application, the Examiner is encouraged to call the undersigned at the number listed below.

Respectfully submitted,

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